

0570  
0102OIPK  
KJCRF Processing Date: 1/15/2002 3:29:02  
Edited by:  
Verified by: (STIC staff)

Serial Number: 09/918,026A

 Changed a file from non-ASCII to ASCII

ENTERED

 Changed the margins in cases where the sequence text was wrapped down to the next line. Edited a format error in the Current Application Data section, specifically: Edited the Current Application Data section with the actual current number. The number inputted by the applicant was  the prior application data; or  other \_\_\_\_\_. Added the mandatory heading and subheadings for "Current Application Data". Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer. Changed the spelling of a mandatory field (the headings or subheadings), specifically: Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted:  non-ASCII "garbage" at the beginning/end of files;  secretary initials/filename at end of file;  
 page numbers throughout text;  other invalid text, such as \_\_\_\_\_. Inserted mandatory headings, specifically: Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: Other:

OIPE

RAW SEQUENCE LISTING DATE: 01/15/2002  
 PATENT APPLICATION: US/09/918,026A TIME: 20:21:04

Input Set : A:\PTO.AMC.txt  
 Output Set: N:\CRF3\01152002\I918026A.raw

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4 <110> APPLICANT: Rosanne M. Crooke
5           Mark J. Graham
6           Kristina M. Lemonidis
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF ACYL COA CHOLESTEROL
ACYLTRANSFERASE-2 EXPRESSION
11 <130> FILE REFERENCE: ISPH-0588
13 <140> CURRENT APPLICATION NUMBER: US/09/918,026A
14 <141> CURRENT FILING DATE: 2001-07-30
16 <160> NUMBER OF SEQ ID NOS: 65
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 20
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21 <213> ORGANISM: Artificial Sequence
23 <220> FEATURE:
24 <223> OTHER INFORMATION: Antisense Oligonucleotide
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32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
35 <223> OTHER INFORMATION: Antisense Oligonucleotide
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43 <213> ORGANISM: Homo sapiens
45 <220> FEATURE:
46 <221> NAME/KEY: CDS
47 <222> LOCATION: (1)...(1569)
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54 gga ggg gag cgg gag cgc caa ccc tgt gga gat gga aac act gag acg   96
55 Gly Gly Arg Glu Arg Gln Pro Cys Gly Asp Gly Asn Thr Glu Thr
56   20          25          30
58 cac aga gcc ccg gac ttg gta caa tgg acc cga cac atg gag gct gtg  144
59 His Arg Ala Pro Asp Leu Val Gln Trp Thr Arg His Met Glu Ala Val
60   35          40          45
62 aag gca caa ttg ctg gag caa gcg cag gga caa ctg agg gag ctg ctg  192
63 Lys Ala Gln Leu Glu Gln Ala Gln Gly Gln Leu Arg Glu Leu Leu
64   50          55          60
66 gat cgg gcc atg cgg gag gct ata caa tcc tac cca tca caa gac aaa  240
67 Asp Arg Ala Met Arg Glu Ala Ile Gln Ser Tyr Pro Ser Gln Asp Lys
68   65          70          75          80

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71	Pro	Leu	Pro	Pro	Pro	Pro	Pro	Gly	Ser	Leu	Ser	Arg	Thr	Gln	Glu	Pro	
72																95	
74	tcc	ctg	ggg	aaa	cag	aaa	gtt	ttc	atc	atc	cgc	aag	tcc	ctg	ctt	gat	336
75	Ser	Leu	Gly	Lys	Gln	Lys	Val	Phe	Ile	Ile	Arg	Lys	Ser	Leu	Leu	Asp	
76																110	
78	gag	ctg	atg	gag	gtg	cag	cat	ttc	cgc	acc	atc	tac	cac	atg	ttc	atc	384
79	Glu	Leu	Met	Glu	Val	Gln	His	Phe	Arg	Thr	Ile	Tyr	His	Met	Phe	Ile	
80																125	
82	gct	ggc	ctg	tgt	gtc	ttc	atc	atc	agc	acc	ctg	gcc	atc	gac	ttc	att	432
83	Ala	Gly	Leu	Cys	Val	Phe	Ile	Ile	Ser	Thr	Leu	Ala	Ile	Asp	Phe	Ile	
84																140	
86	gat	gag	ggc	agg	ctg	ctg	ctg	gag	ttt	gac	cta	ctg	atc	ttc	agc	ttc	480
87	Asp	Glu	Gly	Arg	Leu	Leu	Leu	Glu	Phe	Asp	Leu	Leu	Ile	Phe	Ser	Phe	
88																160	
90	gga	cag	ctg	cca	ttg	gcg	ctg	gtg	acc	tgg	gtg	ccc	atg	ttt	ctg	tcc	528
91	Gly	Gln	Leu	Pro	Leu	Ala	Leu	Val	Thr	Trp	Val	Pro	Met	Phe	Leu	Ser	
92																175	
94	acc	ctg	ttg	gcg	ccg	tac	cag	gcc	cta	cgg	ctg	tgg	gcc	agg	ggc	acc	576
95	Thr	Leu	Leu	Ala	Pro	Tyr	Gln	Ala	Leu	Arg	Leu	Trp	Ala	Arg	Gly	Thr	
96																190	
98	tgg	acg	cag	gcg	acg	ggc	ctg	ggc	tgt	gcg	ctt	tta	gcc	gcc	cac	gcc	624
99	Trp	Thr	Gln	Ala	Thr	Gly	Leu	Gly	Cys	Ala	Leu	Leu	Ala	Ala	His	Ala	
100																205	
102	gtg	gtg	ctc	tgc	gcf	ctg	ccg	gtc	cac	gtg	gcc	gtg	gag	cat	cag	ctc	672
103	Val	Val	Leu	Cys	Ala	Leu	Pro	Val	His	Val	Ala	Val	Glu	His	Gln	Leu	
104																220	
106	ccg	ccg	gcc	tcc	cgt	tgt	gtc	ctg	gtc	ttc	gag	cag	gtt	agg	ttc	ctg	720
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112																255	
114	gcc	aga	cga	ggt	gag	ggg	atc	cag	gcc	ccc	agt	ttc	tcc	agc	tac	ctc	816
115	Ala	Arg	Arg	Gly	Glu	Gly	Ile	Gln	Ala	Pro	Ser	Phe	Ser	Ser	Tyr	Leu	
116																270	
118	tac	tcc	ttc	tgc	cca	aca	ctc	atc	tac	agg	gag	act	tac	cct	agg	864	
119	Tyr	Phe	Leu	Phe	Cys	Pro	Thr	Leu	Ile	Tyr	Arg	Glu	Thr	Tyr	Pro	Arg	
120																285	
122	acg	ccc	tat	gtc	agg	tgg	aat	tat	gtg	gcc	aag	aac	ttt	gcc	cag	gcc	912
123	Thr	Pro	Tyr	Val	Arg	Trp	Asn	Tyr	Val	Ala	Lys	Asn	Phe	Ala	Gln	Ala	
124																300	
126	ctg	gga	tgt	gtg	ctc	tat	gcc	tgc	ttc	atc	ctg	ggc	cgc	ctc	tgt	gtt	960
127	Leu	Gly	Cys	Val	Leu	Tyr	Ala	Cys	Phe	Ile	Leu	Gly	Arg	Leu	Cys	Val	
128																320	
130	cct	gtc	ttt	gcc	aac	atg	agc	cga	gag	ccc	ttc	agc	acc	cgt	gcc	ctg	1008
131	Pro	Val	Phe	Ala	Asn	Met	Ser	Arg	Glu	Pro	Phe	Ser	Thr	Arg	Ala	Leu	
132																335	
134	gtg	ctg	ctc	tct	atc	ctg	cat	gcc	acg	ttg	cca	ggc	atc	ttc	atg	ctg	1056

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135	Val	Leu	Ser	Ile	Leu	His	Ala	Thr	Leu	Pro	Gly	Ile	Phe	Met	Leu	Leu	
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138	ctc	atc	ttc	ttt	gcc	ttc	ctc	cat	tgc	tgg	ctc	aac	gcc	ttt	gcc	gag	1104
139	Leu	Ile	Phe	Phe	Ala	Phe	Leu	His	Cys	Trp	Leu	Asn	Ala	Phe	Ala	Glu	
140					355				360					365			
142	atg	cta	cga	ttt	gga	gac	agg	atg	ttc	tac	cgg	gac	tgg	tgg	aac	tca	1152
143	Met	Leu	Arg	Phe	Gly	Asp	Arg	Met	Phe	Tyr	Arg	Asp	Trp	Trp	Asn	Ser	
144					370				375					380			
146	acg	tcc	ttc	tcc	aac	tac	tac	cgc	act	tgg	aac	gtg	gtg	gtc	cat	gac	1200
147	Thr	Ser	Phe	Ser	Asn	Tyr	Tyr	Arg	Thr	Trp	Asn	Val	Val	Val	His	Asp	
148	385					390					395				400		
150	tgg	ctg	tac	agc	tac	gtg	tat	cag	gat	ggg	ctg	cgg	ctc	ctt	ggt	gcc	1248
151	Trp	Leu	Tyr	Ser	Tyr	Val	Tyr	Gln	Asp	Gly	Leu	Arg	Leu	Leu	Gly	Ala	
152						405				410				415			
154	cgg	gcc	cga	ggg	gta	gcc	atg	ctg	ggt	gtg	ttc	ctg	gtc	tcc	gca	gtg	1296
155	Arg	Ala	Arg	Gly	Val	Ala	Met	Leu	Gly	Val	Phe	Leu	Val	Ser	Ala	Val	
156					420				425					430			
158	gcc	cat	gag	tat	atc	ttc	tgc	ttc	gtc	ctg	ggg	ttc	ttc	tat	ccc	gtc	1344
159	Ala	His	Glu	Tyr	Ile	Phe	Cys	Phe	Val	Leu	Gly	Phe	Phe	Tyr	Pro	Val	
160					435				440					445			
162	atg	ctg	ata	ctc	ttc	ctt	gtc	att	gga	gga	atg	ttg	aac	ttc	atg	atg	1392
163	Met	Leu	Ile	Leu	Phe	Leu	Val	Ile	Gly	Gly	Met	Leu	Asn	Phe	Met	Met	
164					450				455					460			
166	cat	gac	cag	cgc	acc	ggc	ccg	gca	tgg	aac	gtg	ctg	atg	tgg	acc	atg	1440
167	His	Asp	Gln	Arg	Thr	Gly	Pro	Ala	Trp	Asn	Val	Leu	Met	Trp	Thr	Met	
168	465					470				475				480			
170	ctg	ttt	cta	ggc	cag	gga	atc	cag	gtc	agc	ctg	tac	tgc	cag	gag	tgg	1488
171	Leu	Phe	Leu	Gly	Gln	Gly	Ile	Gln	Val	Ser	Leu	Tyr	Cys	Gln	Glu	Trp	
172						485				490				495			
174	tac	gca	cgg	cgg	cac	tgc	ccc	tta	ccc	cag	gca	act	ttc	tgg	ggg	ctg	1536
175	Tyr	Ala	Arg	Arg	His	Cys	Pro	Leu	Pro	Gln	Ala	Thr	Phe	Trp	Gly	Leu	
176					500				505					510			
178	gtg	aca	cct	cga	tct	tgg	tcc	tgc	cat	acc	tag						1569
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## RAW SEQUENCE LISTING

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\01152002\I918026A.raw

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 213 <400> SEQUENCE: 6  
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 217 <211> LENGTH: 19  
 218 <212> TYPE: DNA  
 219 <213> ORGANISM: Artificial Sequence  
 221 <220> FEATURE:  
 222 <223> OTHER INFORMATION: PCR Primer  
 224 <400> SEQUENCE: 7  
 225 gaaggtgaag gtcggagtc 19  
 227 <210> SEQ ID NO: 8  
 228 <211> LENGTH: 20  
 229 <212> TYPE: DNA  
 230 <213> ORGANISM: Artificial Sequence  
 232 <220> FEATURE:  
 233 <223> OTHER INFORMATION: PCR Primer  
 235 <400> SEQUENCE: 8  
 236 gaagatggtg atgggattc 20  
 238 <210> SEQ ID NO: 9  
 239 <211> LENGTH: 20  
 240 <212> TYPE: DNA  
 241 <213> ORGANISM: Artificial Sequence  
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 246 <400> SEQUENCE: 9  
 247 caagcttccc gttctcagcc 20  
 249 <210> SEQ ID NO: 10  
 250 <211> LENGTH: 1607  
 251 <212> TYPE: DNA  
 252 <213> ORGANISM: Mus musculus  
 254 <220> FEATURE:  
 255 <221> NAME/KEY: CDS  
 256 <222> LOCATION: (30)...(1607)  
 258 <220> FEATURE:  
 259 <221> NAME/KEY: unsure  
 260 <222> LOCATION: (176)  
 261 <223> OTHER INFORMATION: a, c, g or t  
 263 <400> SEQUENCE: 10  
 264 ctgtgtgctg tccgcctcac actggcacc atg cag cca aag gtg ccc cag ctt 53  
 265 Met Gln Pro Lys Val Pro Gln Leu  
 266 1 5

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268	cgg	agg	aga	gaa	ggg	ctg	gga	gag	gag	cag	gag	aag	gga	gcc	cgt	gga	101	
269	Arg	Arg	Arg	Glu	Gly	Leu	Gly	Glu	Gln	Glu	Lys	Gly	Ala	Arg	Gly			
270	10					15					20							
272	gga	gaa	ggg	aac	gca	agg	aca	cac	gga	acc	cca	gac	ttg	gtg	caa	tgg	149	
273	Gly	Glu	Gly	Asn	Ala	Arg	Thr	His	Gly	Thr	Pro	Asp	Leu	Val	Gln	Trp		
274	25					30					35					40		
w-OK	276	act	cga	cat	atg	gag	gct	gtg	aag	acn	cag	ttt	ctg	gag	caa	gca	cag	197
277	Thr	Arg	His	Met	Glu	Ala	Val	Lys	Thr	Gln	Phe	Leu	Glu	Gln	Ala	Gln		
278						45					50					55		
280	aga	gag	ttg	gca	gag	ctg	ttg	gat	cg	gcc	cta	tgg	gag	gct	atg	caa	245	
281	Arg	Glu	Leu	Ala	Glu	Leu	Leu	Asp	Arg	Ala	Leu	Trp	Glu	Ala	Met	Gln		
282						60					65					70		
284	gct	tac	ccc	aaa	caa	gac	aga	cct	ctt	ccc	tcc	gct	gcc	cca	gat	tct	293	
285	Ala	Tyr	Pro	Lys	Gln	Asp	Arg	Pro	Leu	Pro	Ser	Ala	Ala	Pro	Asp	Ser		
286						75					80					85		
288	aca	agc	aag	acc	ccg	gag	tta	cgc	cct	gga	aaa	cg	aaa	gtt	ttc	gtc	341	
289	Thr	Ser	Lys	Thr	Pro	Glu	Leu	Arg	Pro	Gly	Lys	Arg	Lys	Val	Phe	Val		
290						90					95					100		
292	gcc	cgc	aag	tca	ctg	atc	gat	gag	cta	atg	gag	gtg	caa	cat	ttc	cga	389	
293	Ala	Arg	Lys	Ser	Leu	Ile	Asp	Glu	Leu	Met	Glu	Val	Gln	His	Phe	Arg		
294	105					110					115					120		
296	acc	atc	tac	cac	atg	ttc	ata	gco	ggc	cta	tgg	ttc	ttg	atc	atc	agc	437	
297	Thr	Ile	Tyr	His	Met	Phe	Ile	Ala	Gly	Leu	Trp	Phe	Leu	Ile	Ile	Ser		
298						125					130					135		
300	acc	ctg	gcc	atc	gac	ttc	att	gat	gag	ggc	agg	ttg	atg	ctg	gag	ttt	485	
301	Thr	Leu	Ala	Ile	Asp	Phe	Ile	Asp	Glu	Gly	Arg	Leu	Met	Leu	Glu	Phe		
302						140					145					150		
304	gac	tta	ctc	ctc	ttc	agc	ttc	gga	cag	ctg	ccc	ttg	gco	ctg	atg	acc	533	
305	Asp	Leu	Leu	Leu	Phe	Ser	Phe	Gly	Gln	Leu	Pro	Leu	Ala	Leu	Met	Thr		
306						155					160					165		
308	tgg	gtt	ccc	atg	ttc	ctg	tat	acg	ctc	cta	gtg	ccc	tac	cag	acc	ctg	581	
309	Trp	Val	Pro	Met	Phe	Leu	Tyr	Thr	Leu	Leu	Val	Pro	Tyr	Gln	Thr	Leu		
310						170					175					180		
312	tgg	ctg	tgg	gcc	agg	ccg	cgc	gct	ggg	ggt	gcc	tgg	atg	ctg	ggg	gcc	629	
313	Trp	Leu	Trp	Ala	Arg	Pro	Arg	Ala	Gly	Gly	Ala	Trp	Met	Leu	Gly	Ala		
314	185					190					195					200		
316	agc	ctg	ggc	tgc	gtt	ctg	ctg	gct	gcc	cac	gct	gtg	gtg	ctc	tgc	gtc	677	
317	Ser	Leu	Gly	Cys	Val	Leu	Leu	Ala	Ala	His	Ala	Val	Val	Leu	Cys	Val		
318						205					210					215		
320	ctg	ccg	gtg	cac	gtg	tca	gtg	agg	cat	gag	ctt	ccg	ccc	gcc	tgc	gtc	725	
321	Leu	Pro	Val	His	Val	Ser	Val	Arg	His	Glu	Leu	Pro	Pro	Ala	Ser	Arg		
322						220					225					230		
324	tgc	gtg	ctg	gtc	ttt	gag	cag	gtc	aga	ttg	ctg	atg	aaa	agc	tac	tcc	773	
325	Cys	Val	Leu	Val	Phe	Glu	Gln	Val	Arg	Leu	Leu	Met	Lys	Ser	Tyr	Ser		
326						235					240					245		
328	ttc	ctg	aga	gag	act	gtg	cct	ggg	atc	ttt	tgt	gtc	aga	cga	gga	aag	821	
329	Phe	Leu	Arg	Glu	Thr	Val	Pro	Gly	Ile	Phe	Cys	Val	Arg	Arg	Gly	Lys		
330						250					255					260		
332	ggc	atc	agc	ccc	cca	agt	ttc	tcc	agt	tac	ctc	tac	ttc	ctc	tgc		869	

**VERIFICATION SUMMARY**

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L:276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10